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研究報告

1. 新型インフルエンザ流行に対する封じ込め対策の Individual Based Model を用いた効果解析，森本智子，銭花知弘，米谷祐介，石川洋文，日本衛生学雑誌，Vol. 64, No. 2, pp. 442, 2009.
2. 丘陵部におけるガス状物質濃度場の予測，佐々木裕一，水藤寛，第 23 回数値流体力学シンポジウム講演論文集，D4-1，2009.
3. A bias correction and acceleration approach for the problem of regions, Masao Ueki and Kaoru Fueda, Journal of Statistical Planning and Inference, Vol. 139, No. 10, pp. 3533-3542, 2009.
4. Modeling the Dynamics and Control of Transmission of *Schistosoma japonicum* and *S. mekongi* in Southeast Asia, Hirofumi Ishikawa and Hiroshi Ohmae, The Korean Journal of Parasitology. Vol. 47, No. 1, pp. 1–5, 2009.
5. Risk assessment of re-emerging *Plasmodium falciparum* on Ishigaki Island using a stochastic transmission model, Yuuki Nakagawa, Masao Ueki, Kaoru Fueda, Hiroshi Ohmae and Hirofumi Ishikawa, Tropical Medicine and Health Vol.37 No. 3, pp 97-107, 2009.
6. A dengue transmission model in Thailand considering sequential infections with all four serotypes, Eriko Chikaki and Hirofumi Ishikawa, The Journal of Infection in Developing Countries, Vol. 3, No. 9, pp. 711-722, 2009.
7. Effectiveness assessment of countermeasures against bioterrorist smallpox attacks in Japan using an individual-based model, Tomohiro Zenihana and Hirofumi Ishikawa, Environmental Health and Preventive Medicine, Vol. 15, No. 2, pp. 84-93, 2010.
8. The Prospects of *Plasmodium vivax* Malaria Invading Himi-shi, Toyama Prefecture, Japan, Tomoyuki Bitoh, Yuhki Nakagawa, Masao Ueki, Kaoru Fueda, Hiroshi Ohmae and Hirofumi Ishikawa, Journal of International Health. Vol. 24, No. 3, pp. 219, 2009.
9. Global stability of pathogen-immune dynamics with absorption, Tsuyoshi Kajiwara and Toru Sasaki, Journal of Biological Dynamics, published online, 2009.
10. Global stability of models of humoral immunity against multiple viral strains, Toru Inoue, Tsuyoshi Kajiwara and Toru Sasaki, Journal of Biological Dynamics, published online, 2009.
11. Computational analysis for motions of rugby balls interacting with air flows, Koki Tanino and Hiroshi Suito, Football Science, Vol. 6, pp. 34-38, 2009.
12. Validation of a demand forecasting method based on a stochastic process using real-world data, Yinggao Zheng, Hiroshi Suito and Hideo Kawarada, to be published in Journal of Numerical Mathematics, 2010.

新型インフルエンザ流行に対する封じ込め対策の Individual Based Model を用いた効果解析

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■ 概　要 ■

【目的】近年、新型インフルエンザの原因となる高病原性鳥インフルエンザ(H5N1)が世界各地の家禽や野鳥の間で蔓延し、東南アジアを中心に 2003 年以降 15 カ国で人への感染が確認されている。こうした状況から、世界各国では新型インフルエンザが発生し大流行をまねく可能性に警戒を強めている。過去には“Spanish flu” A (H1N1)、“Asian flu” A (H2N2)、“ Hong Kong flu” A (H3N2)という大きな influenza pandemic が起こっており、最も大きな被害を出した 1918-1919 年“Spanish flu” A (H1N1) では少なくとも 4,000 万人の死亡者を出したと報告されている。本研究ではこれら過去の流行データを用い、新型インフルエンザ発生を想定したシミュレーションを通して、厚生労働省の対策行動計画に基づいた抗インフルエンザ薬タミフルの投与や学級閉鎖、プレパンデミックワクチンの接種による対策の有効性について予測・分析を行う。

【方法】本研究では、現実により近い状況を取り扱うために、個々人に年齢、居住区、家族、所属する mixing group などの情報を与える Individual Based Model を用いる。これによってシミュレーションを行う仮想地域における住民それぞれの感染状況を確率的に扱うことができる。研究対象地は北海道札幌市に設定し、同市の人口統計に基づいて住民情報を構築する。過去の influenza pandemic では、子供の間での発病率が非常に高かった。また、学校に通う子供の間では密接な接触を行う機会が多いことから、子供が感染拡大の原因となることが考えられる。本研究では子供の間での感染に注目し、学齢児童を対象に学校ごとに抗ウイルス薬の投与を行う School-age Targeted Antiviral Prophylaxis (STAP) や、厚生労働省による対策行動計画に基づき学校閉鎖を行った場合についてシミュレーションを行い、感染封じ込めに対しての効果を分析する。また、対策行動計画に基づき感染者とその接触者に抗ウイルス薬の投与を行う Targeted Antiviral Prophylaxis(TAP) や、地域ごとに投与を行う Geographical Targeted Antiviral Prophylaxis(GTAP)、プレパンデミックワクチンの接種による対策を考える。

【結果】上述の各対策に対するシミュレーションを行い、感染流行の様子を比較する。さらに、総感染者数や年齢別罹患率、投薬量に基づき対策有効性を分析する。シミュレーションの結果、感染者数や抗ウイルス薬投薬数の点から、対策行動計画の方針である TAP が最も有効な対策であることが確認できた。また STAP や学校閉鎖は、子供の罹患率を大きく減少させ、ひいては全住民に対する感染封じ込めにつながった。

■キーワード■
新型インフルエンザ, A(H5N1), Individual-based-model (IBM), 抗ウイルス薬投与, 札幌市

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丘陵部におけるガス状物質濃度場の予測

佐々木　裕一[1)]，水藤　寛[2,3)]

■　概　要　■

今日、工場や廃棄物処理施設など多くの焼却炉が私たちの生活圏内に存在する。これらの焼却炉から排出される汚染物質は人や環境に悪影響を与える可能性があり、私たちが安心して生活するためには、汚染物質による周辺への影響を予測し、予防・対策を行うことが重要となる。本研究では、大気汚染を対象とした環境影響評価に役立てることを目的として、風向・風速、気温などのデータを用いてガス状物質の移流・拡散についてのシミュレーションを行った。また、シミュレーション結果からガスの地上濃度場を求め、日本原子力研究所によって行われ、公表されている狭域野外拡散試験データ（筑波 90）における拡散試験結果との比較を行った。

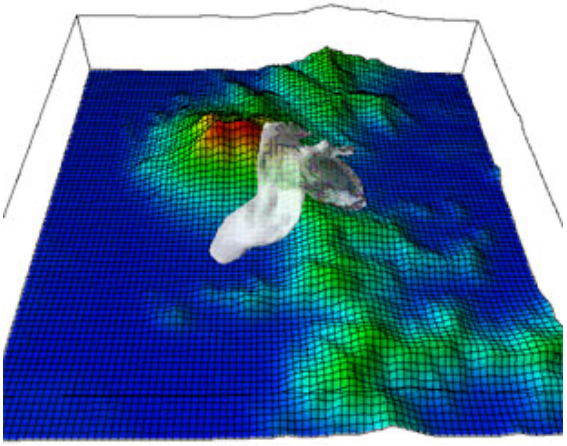

図１　RUN1 における汚染物質濃度の等値面

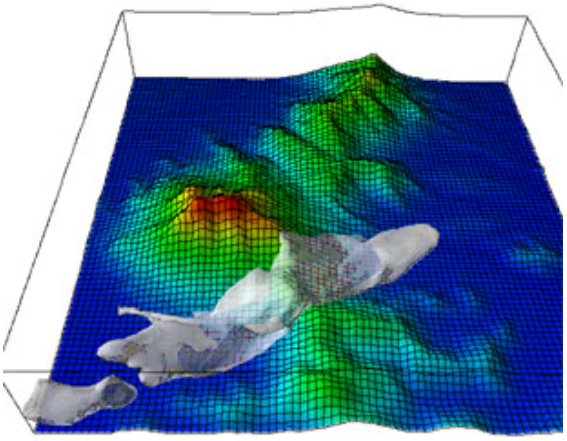

図２　RUN2 における汚染物質濃度の等値面

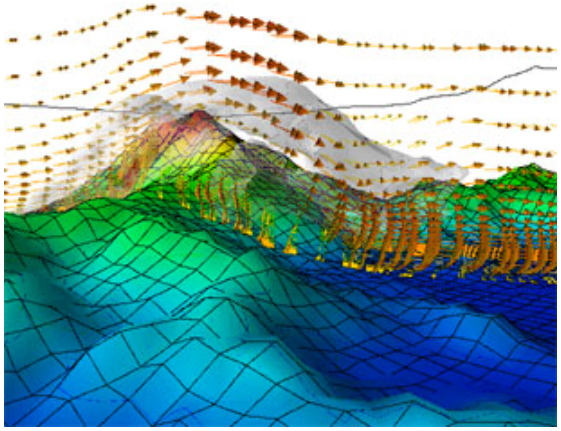

図３　山頂付近における流速場と濃度等値面

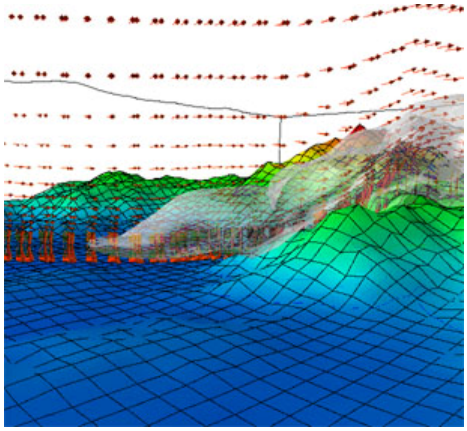

図４　放出位置付近の流速場と濃度等値面

■キーワード■

数値シミュレーション、大気汚染、環境影響評価

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査読：なし，言語：日本語

A bias correction and acceleration approach for the problem of regions

Masao Ueki[1,✍)] and Kaoru Fueda[2)],

■ **Summary**■

For testing the problem of regions in the space of distribution functions, this paper considers approaches to modify the bootstrap probability to be a second-order accurate p-value based on the familiar bias correction and acceleration method. It is shown that Shimodaira's [2004. Approximately unbiased tests of regions using multistep-multiscale bootstrap resampling. Ann. Statist. 32, 2616-2641] twostep-multiscale bootstrap method works even in the problem of regions in functional space. In this paper the bias correction quantity is estimated by his onestep-multiscale bootstrap method. Instead of using the twostep-multiscale bootstrap method, the acceleration constant is estimated by a newly proposed jackknife method which requires first-level bootstrap resamplings only. Some numerical examples are illustrated, in which an application to testing significance in model selection is included.

取り扱っている問題

統計学で最も一般的に用いられている検定問題は、観測対象母集団の平均、分散などの値に関して、それがある基準値より有意に大きいか、あるいは多少大きくてもバラツキの範囲内なのか、といった判断を下す。本論文で扱っている problem of regions とは、母集団の確率分布が、ある集合に入っているか否かという判断を下す問題である。

適用例

多変量解析における変数選択などのモデル選択においては、AIC (Akaike Information Criterion: 赤池情報量規準:故赤池先生御本人は A Information Criterion と書かれていた)やそれを一般化した GIC (Generalized Information Criterion)が用いられる。problem of regions は、選ばれたモデルが他のモデルよりも有意に適しているかの検定に用いることができる。

本論文の成果

検定は p-value を計算し、それが予め定めた有意水準より小さい場合に仮説を棄却することで行われる。従って p-value の計算は極めて重要である。本論文が提案する方法は従来の方法より高精度に p-value を計算できることを、理論的に証明し、さらにいくつかのシミュレーションによって確認した。

■**Key word**■

Bias correction and acceleration, Edgeworth expansion, jackknife method, multiscale-multistep bootstrap method, problem of regions, second-order unbiased p-value, significance of model selection

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Modeling the Dynamics and Control of Transmission of Schistosoma japonicum and S. mekongi in Southeast Asia

Hirofumi Ishikawa[1,2,*)] and Hiroshi Ohmae[3)]

■ **Summary**■

A mathematical model for transmission of schistosomes is useful to predict effects of various control measures on suppression of these parasites. This review focuses on epidemiological and environmental factors in *Schistosoma japonicum* and *Schistosoma mekongi* infections and recent advances in mathematical models of *Schistosoma* transmission.

■**Key word**■

Schistosoma japonicum, *Schistosoma mekongi*, mathematical model, control strategies

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doi: 10.3347/kjp.2009.47.1.1.

Refreeing: Mini Review, Language: English

Risk assessment of re-emerging Plasmodium falciparum on Ishigaki Island using a stochastic transmission model

Yuuki Nakagawa[1,✍)], Masao Ueki[2,✍✍)], Kaoru Fueda[1,3)], Hiroshi Ohmae[4)] and Hirofumi Ishikawa[1,5,*)]

■ **Summary**■

On Ishigaki Island, *Plasmodium falciparum* and *Plasmodium vivax* epidemics occurred in 1945-1946 and were successfully suppressed. The epidemic re-emerged in 1949 because many settlers immigrated to the former endemic areas, but it terminated in 1961. The present study aimed at predicting an outbreak of a new epidemic based on the situation in which *P. falciparum* malaria patients stay on Ishigaki Island and also examined the re-emergence of the *P. falciparum* epidemic in 1951-1960 to determine the reliability of the model.

A stochastic transmission model of *P. falciparum* was constructed to detect a small number of infected persons. The seasonal fluctuation of the *Anopheles minimus* population obtained by observational data and meteorological data through statistical processing was introduced into the model.

Simulations were carried out to predict the risk of a new epidemic with scenarios in which the attribute of index patient, visiting season, and reduced inoculation rates of *An. minimus* were assumed. When an infected person visited the island in summer, a small number of patients with primary infections derived from the index patient appeared for all 1,000-iterations. On the other hand, when an infected person visited the island in winter, few or no patients with primary infections appeared for any of the 1,000-iterations because of the low mosquito density. In realistic conditions, the simulation results showed that there was little possibility of the occurrence of *P. falciparum* infection.

■**Key word**■

Plasmodium falciparum, *Anopheles minimus*, Ishigaki Island, re-emergence, stochastic simulation

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■**Printing**■

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Refreeing: Original article, Language: English

A dengue transmission model in Thailand considering sequential infections with all four serotypes

Eriko Chikaki[1)] and Hirofumi Ishikawa[1,2,*)]

■ **Summary**■

Background: Dengue fever/dengue haemorrhagic fever is prevalent in Thailand, where all serotypes are found and the dominant serotype has changed irregularly. Although almost all primary infections present with slight symptoms or are asymptomatic, little is known about the infectiousness of dengue fever.

Methodology: A mathematical model of the transmission for dengue virus was constructed covering the possibility of sequential infections with all four different serotypes. The model was combined with the seasonal population dynamics of *Aedes aegypti*, the principal vectors of dengue virus in Thailand. The contributions of inapparent cases in the transmission to mosquito vectors and antibody-dependent enhancement were incorporated into the model. Moreover, the hypothesis of an "unnatural" infection route was examined, where a person acquires immunity by infection during a cross-immunity period, through model simulations.

Results: A comparative study on the transmission probabilities of inapparent cases to mosquito vectors showed that the prevalence of dengue infection could be immediately stamped out after a severe outbreak if inapparent cases had no infectiousness. The simulation under an "unnatural" infection route assumption resulted of yearly changes in the dominant serotype and sharp, irregular variations in outbreaks.

Conclusion: The supposition that inapparent cases had no infectiousness was not in accord with the actual situation in Thailand. Furthermore, the simulation result supported the "unnatural" infection route as having an influence on epidemics of dengue.

■**Key word**■
dengue, inapparent infection, Thailand, antibody-dependent-enhancement, mathematical model

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Refreeing: Original article, Language: English

Effectiveness assessment of countermeasures against bioterrorist smallpox attacks in Japan using an individual-based model

Tomohiro Zenihana[1)] and Hirofumi Ishikawa[1,2,*)]

■ **Summary**■

Objectives: This study is aimed at the evaluation of countermeasures in terms of the total number of patients and deaths, the number of vaccine doses used, and the time for eradication as examined through simulations of the outbreak of smallpox following a bioterrorist attack in the center of Okayama City. Three countermeasures were considered: traced vaccination (TV), mass vaccination (MV), and school closure.

Methods: An individual-based model was adopted, in which every individual is assigned their own personal information, behavioral pattern, and interactions among social settings to simulate the situation on a realistic basis. The influence of residual immunity obtained by past vaccination reflected age-dependent immunity to smallpox in Japan.

Results: MV performed within a 2-day period at the same time in 10 school districts had the highest effectiveness in reducing the total number of patients and deaths among all simulations. Performing both TV and MV simultaneously was much more effective than performing TV or MV individually. The decrease in the number of patients with TV or MV in combination with school closure was faster than that by TV or MV without school closure.

Conclusions: According to the simulations results, it was advisable to carry out MV, or both TV and MV, simultaneously with school closure as countermeasures against a smallpox epidemic initiated by a bioterrorist attack.

■**Key word**■
Smallpox, Bioterrorism, Individual-based model (IBM), Residual immunity, Countermeasures

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The Prospects of Plasmodium vivax Malaria Invading Himi-shi, Toyama Prefecture, Japan

Tomoyuki Bitoh[1)], Yuhki Nakagawa[1)], Masao Ueki[2)], Kaoru Fueda[1,3)], Hiroshi Ohmae[4)] and Hirofumi Ishikawa[1,5)]

■ **Summary**■

Background: There have been no reports of domestic infection by *Plasmodium vivax* in Japan since *P. vivax* was eradicated in the 1960s. However, about 30 patients infected by *P. vivax* overseas are detected annually. In 2004 the Toyama Institute of Public Health observed habitations of *Anopheles sinensis* in Toyama Prefecture. Therefore, there is a possibility of *P. vivax* malaria re-emerging and becoming endemic, due to these infected visitors and returnees.

Aims: We chose Himi-shi, Toyama, as the study area to examine the re-emergence of *P. vivax* and the observational data of vectors. We developed a mathematical model that can estimate the prevalence of *P. vivax* malaria infected visitors to predict the risk of *P. vivax* malaria invasion.

Methods: We constructed a stochastic model for the transmission of *P. vivax* malaria able to register any small increases in infections. During the transmission cycle, there are two kind of hosts; mosquito vectors (*An. sinensis*) and humans.
(1) Vectors: the period of the formation of sporozoites in mosquitoes, the daily survival rate, and the possibility of infected mosquitoes injecting sporozoites into local residents, were assumed to follow the standard probability distributions.
(2) Humans: we took the process of developing symptoms and changes in the diagnostic period into consideration. The incubation period for primary infection, the relapse period, the rate of transfer to gametocytes and the rate of gametocyte loss were assumed to follow standard probability distributions. The mean diagnostic period was set at 20 days at the beginning but was assumed to shorten with the progression of *P. vivax* epidemic.

Results and Conclusions: If a tourist infected with *P. vivax* visited in the summer, the infection risk to local residents was assessed as 0.19% at most even if the human bait index of *An. sinensis* were estimated very highly at 10%. If 20 refugees infected with *P. vivax* drifted ashore, the risk was assessed at 1.95%, resulting in the slight possibility of an outbreak of a *P. vivax* malaria epidemic.

■**Key word**■
re-emergence, *Plasmodium vivax*, *Anopheles sinensis*, Toyama, stochastic simulation

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4) Department of Parasitology, National Institute of Infectious Diseases
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■**Printing**■
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49th Congress for Tropical Medicine and Health & 23th Congress for International Health
Refreeing: Abstract for Congress, Language: English

Global stability of pathogen-immune dynamics with absorption

Tsuyoshi Kajiwara[1)] and Toru Sasaki[2)]

■ **Summary**■

In this paper, we consider the global stability of the models which incorporate humoural immunity or cell-mediated immunity. We consider the effect of loss of a pathogen, which is called the absorption effect when it infects an uninfected cells. We construct Lyapunov functions for these models under some conditions of parameters, and prove the global stability of the interior equilibria. It is impossible to remove the condition of parameters for the model incorporating humoural immunity.

■**Key word**■
immunity, global stability, Lyapunov function, absorption

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■**Printing**■
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DOI: 10.1080/17513750903051989
Refreeing: Original article, Language: English

Global stability of models of humoral immunity against multiple viral strains

Toru Inoue[1)], Tsuyoshi Kajiwara[2)] and Toru Sasaki[3)]

■ **Summary**■

We analyse, from a mathematical point of view, the global stability of equilibria for models describing the interaction between infectious agents and humoral immunity. We consider the models that contain the variables of pathogens explicitly. The first model considers the situation where only a single strain exists. For the single strain model, the disease steady state is globally asymptotically stable if the basic reproductive ratio is greater than one. The other models consider the situations where multiple strains exist. For the multi-strain models, the disease steady state is globally asymptotically stable. In the model that does not explicitly contain an immune variable, only one strain with the maximum basic reproductive ratio can survive at the steady state. However, in our models explicitly involving the immune system, multiple strains coexist at the steady state.

■**Key word**■
humoral immunity, multiple strains, global stability, Lyapunov function, LaSalle's invariance principle

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■**Printing**■
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Computational analysis for motions of rugby balls interacting with air flows

Koki Tanino[1)] and Hiroshi Suito[1,2)]

■**Summary**■

Computational simulations of motions of rugby balls are presented. Fluid-structure interaction plays an important role in the motion of rugby balls. Incompressible Navier-Stokes equation is solved on a Cartesian coordinate system, and the motions of rugby balls are calculated by Newton's equation of motion for transitional motion and Euler's equation of motion for the rotation simultaneously. Computational results are compared with experiments for screw and high punt kick cases.

Fig. 1 Screw kick

Fig. 2 High punt kick

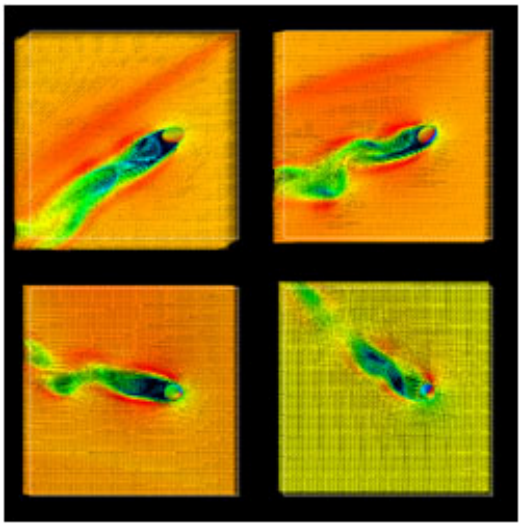

Fig. 3 Simulation result for screw kick

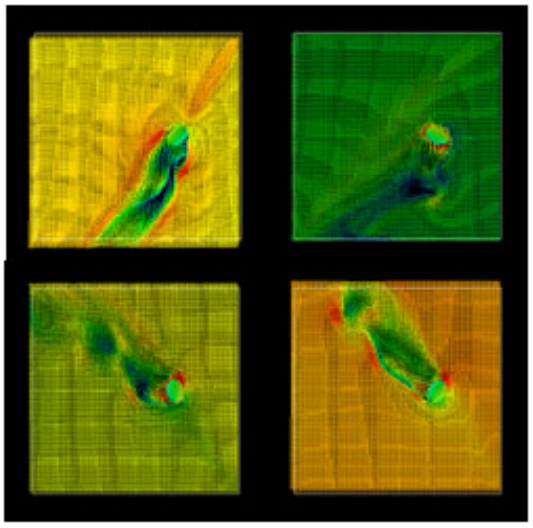

Fig. 4 Simulation result for high punt kick

■**Key word**■

computational fluid dynamics, fluid-structure interaction, screw kick, high punt kick

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Validation of a demand forecasting method based on a stochastic process using real-world data

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■ **Summary**■

Demand-forecasting problems frequently arise in logistics and supply chain management. The Newsboy Problem is one such problem. In this paper, we present an improved solution method by application of the Black-Scholes model incorporating a stochastic process used in financial engineering for option pricing. The proposed model is shown to be effective through numerical experiments using real-world data.

In demand-forecasting problems, the quantity of expected demand and the most suitable wholesale quantity are sought. These important problems in the field of Effective Demand Management have appeared also in the fields of logistics and supply chain management. Demand-forecasting systems should support the purchasing and sales departments of companies. They are intended to reduce differences between sales and demand. In recent years, various means have been adopted to determine quantities of demand and optimal wholesale size. In contrast, few studies have examined Newsboy Problems (NBPs). Commodities of some kinds become worthless after a certain time passes, e.g. newspapers and perishable foods. For stock control of such commodities, the daily decision for wholesale quantity becomes an important problem.

Problems of these kinds are designated as Newsboy Problems. Kawarada and Hachiya reformulated it using the Martingale theory and the Black-Scholes model ("Optimal stock control strategy based on stochastic process", Journal of Logistics and Informatics, Vol. 1, No. 1, pp. 39-47, 2004). In this formulation, the Black-Scholes model, which is widely used in financial engineering, is adopted, in which opportunity and disposal losses correspond respectively to call and put options. In this paper, we present practical methods of finding an optimal wholesale quantity. Then we evaluate it through numerical experiments using time series data in a retail shop.

■**Key word**■
demand prediction, stochastic process, Newsboy Problem, Black--Scholes model, Loss evaluation

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